## SEQUENCE LISTING <110> CJ Corporation <120> An alkaline lipase from Vibrio metschnikovii RH530 and a nucleotide sequence encoding the same <160> 5 <170> KopatentIn 1.71 <210> 2578 <211> <212> DNA Vibrio metschnikovii RH530 <213> <400> agcttgcact ttatcagcca atacttgcat cggtaactcg gcgggcactt gtgcccagtg 60 120 gcqqcqqcta cqtacttcaq agattaaggc catgactagc gtttcatata aaatggtgtc 180 tcgccacqta ccttqaatqq cqatacqcaq ctqqcqtttq ccctcttqct tgaggatccc gatttcaatt tgccgatcgg gttgaaaatg gaaatagcgt aatgactgta aaaaagtacg 240 300 attcaaatqa qqtqcatqct qctctaaata aacaatqtcg gcatccgaaa agcgcaatga 360 agccaactga ttgatttctt ggcgtacttc ctctaataaa tcgctaatgt cttcatcact 420 qcqcacaatc aattcatagc qcacctcaac atccggatac aacgaatgaa cggcctgcat 480 catattgatt ttataggcat caagatccaa taaactgcgg ataaaaagag gagaaaatag qcqatcqctc atqatqatqc catcctttcq ttcggtttca ttcagtcatt acgttagtaa 540 600 caacqtqttq ctaactttqq qcqaacaata aaqtaccctt gtaaqtttgt caacttttgt qacaaaccta qtcaqtcqtt atttqqcctt attataatta tggatattga ggggtaagga 660 720 cgtagtcata acaacaatta cagtactctt gttatctgag ttatgtttgt cacaaagtct tatttacatt tgaccatcat catgcactta cctaaaataa gcccgttgtt tattagggaa 780 gccattatga ttgtcactat cgatatgatt tgtctgcgtc ttgcgccgaa atctatccag 840 900 gttttactgg tgaaacgctc taatccaaat cggccagatt gtggtaaatg ggcattgcct 960 gqcqqqataq tqtatqacqa agatatqacc gctcatggtg gagaacctgt cgatgaggat 1020 tttgatgcag cgagacgacg tatttgtcgg caaaaagtcc atacttatcc taattttatc agcgatccgc tggttgatgg caaccccaaa cgcgatccga atggttggag tgtcagtatt 1080 1140 tcccattacg ctttattaaa cccgtggaat gtcaaacaaa tagaagattt tggtatcgac 1200 cccqaqcqcq ctaattqqtt tqatcttcat actttactca aagaagaaat gccgctggct 1260 tttgatcatg tcgcgcaaat tcagcatgcg tggcaaaaat tacgcgctgc ggttgaatac 1320 acatccqtqq tactattttc attagaaaaa qagtttttag tggcggatat tattgatgcc tacgccaaat ttggcgtcga agttaatcgc atgaccatta aacgccgctt gatcaatacc 1380 ggggtgatcg tcagtaccaa taaaatggcc gcatcttgta aaggcaaagg agccaaacca 1440

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cct aaa ata agc ccg Pro Lys Ile Ser Pro I 20	eu Phe Ile A <u>r</u>	gg gaa gcc rg Glu Ala 25	att atg att Ile Met Ile 30	· Val Thr	96				
atc gat atg att tgt of Ile Asp Met Ile Cys I					144				

ctg Leu	gtg Val 50	aaa Lys	cgc Arg	tct Ser	aat Asn	cca Pro 55	aat Asn	cgg Arg	cca Pro	gat Asp	tgt Cys 60	ggt Gly	aaa Lys	tgg Trp	gca Ala	192
ttg Leu 65	cct Pro	ggc Gly	ggg Gly	ata Ile	gtg Val 70	tat Tyr	gac Asp	gaa Glu	gat Asp	atg Met 75	acc Thr	gct Ala	cat His	ggt Gly	gga Gly 80	240
gaa Glu	cct Pro	gtc Val	gat Asp	gag Glu 85	gat Asp	ttt Phe	gat Asp	gca Ala	gcg Ala 90	aga Arg	cga Arg	cgt Arg	att Ile	tgt Cys 95	cgg Arg	288
caa Gln	aaa Lys	gtc Val	cat His 100	act Thr	tat Tyr	cct Pro	aat Asn	ttt Phe 105	atc Ile	agc Ser	gat Asp	ccg Pro	ctg Leu 110	gtt Val	gat Asp	336
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tac Tyr	gct Ala 130	tta Leu	tta Leu	aac Asn	ccg Pro	tgg Trp 135	aat Asn	gtc Val	aaa Lys	caa Gln	ata Ile 140	gaa Glu	gat Asp	ttt Phe	ggt Gly	432
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gaa Glu	gaa Glu	atg Met	ccg Pro	ctg Leu 165	gct Ala	ttt Phe	gat Asp	cat His	gtc Val 170	gcg Ala	caa Gln	att Ile	cag Gln	cat His 175	gcg Ala	528
tgg Trp	caa Gln	aaa Lys	tta Leu 180	cgc Arg	gct Ala	gcg Ala	gtt Val	gaa Glu 185	tac Tyr	aca Thr	tcc Ser	gtg Val	gta Val 190	cta Leu	ttt Phe	576
tca Ser	tta Leu	gaa Glu 195	aaa Lys	gag Glu	ttt Phe	tta Leu	gtg Val 200	gcg Ala	gat Asp	att Ile	att Ile	gat Asp 205	gcc Ala	tac Tyr	gcc Ala	624
aaa Lys	ttt Phe 210	ggc Gly	gtc Val	gaa Glu	gtt Val	aat Asn 215	cgc Arg	atg Met	acc Thr	att Ile	aaa Lys 220	cgc Arg	cgc Arg	ttg Leu	atc Ile	672
aat Asn 225	acc Thr	ggg Gly	gtg Val	atc Ile	gtc Val 230	agt Ser	acc Thr	aat Asn	aaa Lys	atg Met 235	gcc Ala	gca Ala	tct Ser	tgt Cys	aaa Lys 240	720
ggc Gly	aaa Lys	gga Gly	gcc Ala	aaa Lys 245	cca Pro	gcc Ala	acc Thr	gtt Val	tat Tyr 250	cgt Arg	ctt Leu	gcc Ala	agt Ser	cat His 255	gaa Glu	768
								cga Arg 265								798

<sup>&</sup>lt;210> 3 <211> 266 <212> PRT <213> Vibrio metschnikovii RH530

<sup>&</sup>lt;400> 3 Met Phe Val Thr Lys Ser Tyr Leu His Leu Thr Ile Ile Met His Leu Page 3

5 10 15

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<sup>&</sup>lt;211> 555

<sup>&</sup>lt;212> DNA <213> Vibrio metschnikovii RH530

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (1)..(555) <223> valL2 gene

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att agc tac aac tca ctc gct atc gat gat gag gcc att ttt cgc cgc Ile Ser Tyr Asn Ser Leu Ala Ile Asp Asp Glu Ala Ile Phe Arg Arg 35 40 45	144							
ctt gac cga tcg ctc act cat gcc tcg cct aat gct tta gtc gga cac Leu Asp Arg Ser Leu Thr His Ala Ser Pro Asn Ala Leu Val Gly His 50 55 60	192							
agt ttg ggc gga ttg gtg atc aaa cgt tat cta gaa tcg cgc gca ccg Ser Leu Gly Gly Leu Val Ile Lys Arg Tyr Leu Glu Ser Arg Ala Pro 65 70 75 80	240							
tcc tgt gaa acc ctc tcc cat gtc gtc gcc atc ggc tca cct ttg caa Ser Cys Glu Thr Leu Ser His Val Val Ala Ile Gly Ser Pro Leu Gln 85 90 95	288							
gga gct tcc att gtc aat aaa att gag caa tta ggt tta ggg gtg gca Gly Ala Ser Ile Val Asn Lys Ile Glu Gln Leu Gly Leu Gly Val Ala 100 105 110	336							
cta ggt aat tca gca gaa ttt ggg tta aaa gaa cac gac gac gaa tcc Leu Gly Asn Ser Ala Glu Phe Gly Leu Lys Glu His Asp Asp Glu Ser 115 120 125	384							
cgc tat cca caa aaa tca ggc agt att gca gga acg ata cct tta ggg Arg Tyr Pro Gln Lys Ser Gly Ser Ile Ala Gly Thr Ile Pro Leu Gly 130 135 140	432							
ctg cgc agc ctt tta ctg cgc gat cca ctg gac tcc gat ggt acc gtc Leu Arg Ser Leu Leu Leu Arg Asp Pro Leu Asp Ser Asp Gly Thr Val 145 150 155 160	480							
aca gta gaa gaa acc aaa ata gct ggc atg aca gat cat atc gcg ata Thr Val Glu Glu Thr Lys Ile Ala Gly Met Thr Asp His Ile Ala Ile 165 170 175	528							
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Leu Asp Arg Ser Leu Thr His Ala Ser Pro Asn Ala Leu Val Gly His Page 5								